Amendments to the Claims:

Please amend claims 1, 5 and 8. This listing of claims replaces all prior versions and listings of claims in the application:

Listing of Claims:

1. (Currently Amended) A computer-based method for identifying conserved peptide motifs useful as drug targets for use in a host organism, wherein the said method comprises the steps of:

i) ~~providing electronic data representing peptide libraries from the protein sequences of selected organisms,~~

~~ii) from the data of step (i),~~ generating computationally overlapping peptide sequences from selected organisms of length 'N', ~~and~~

(ii) sorting computationally the peptide sequences of length 'N' according to amino acid sequence,

(iii) matching computationally the sorted peptide sequences of length 'N' of the selected organisms to produce matched common peptide sequences,

(iv) locating computationally the matched common peptide sequences in the protein sequences of step i) and subsequently labeling the matched common peptide sequences with their origin and location,

(v) joining computationally overlapping common peptide sequences to obtain extended conserved peptide sequences,

(vi) annotating secondary structure of extended conserved peptide sequences based on a crystal structure database, and

vii) ~~comparing known proteins of a pathogenic organism with those of non-pathogenic organisms using the aforementioned steps (i) to (v), to select at least one conserved peptide~~

~~sequence not commonly conserved in both the pathogenic organism and in non-pathogenic organisms, to obtain a conserved peptide sequence,~~

~~viii) validating computationaly the conserved peptide sequences obtained in step (vii) as a potential drug target sequences by searching for the conserved peptide sequence in a host organism~~ identifying conserved sequences not present in the host organism.

2. (Previously Presented) The method of claim 1 wherein 'N' is at least 4.

3. (Previously Presented) The method of claim 1 wherein the selected organisms include at least one of: Mycoplasma pneumoniae, Helicobacter pylori, Hemophillus influenzae, Mycobacterium tuberculosis, Mycoplasma genitalium, Bacillus subtillis, and Escherichia coli.

4. (Previously Presented) A method as claimed in claim 1 where conserved peptide motifs as modified comprising sequences include one or more of:

1. AAQSIGEPGTQLT (SEQ ID NO:1)
2. AGDGTTTAT (SEQ ID NO:2)
3. AGRHGNKG (SEQ ID NO:3)
4. AHIDAGKTTT (SEQ ID NO:4)
5. CPIETPEG (SEQ ID NO:5)
6. DEPSIGLH (SEQ ID NO:6)
7. DEPTSALD (SEQ ID NO:7)
8. DEPTTALDVT (SEQ ID NO:8)
9. DHAGIATQ (SEQ ID NO:9)
10. DHPHGGGEG (SEQ ID NO10)
11. DLGGGTFD (SEQ ID NO:11)
12. DVLDTWFSS (SEQ ID NO:12)
13. ERERGITI (SEQ ID NO:13)
35. KMSKSKGN (SEQ ID NO:35)
36. KMSKSLGN (SEQ ID NO:36)
37. KNMITGAAQMDGAILVV (SEQ ID NO:37)
38. KPNSALRK (SEQ ID NO:38)
39. LFGGAGVGKTV (SEQ ID NO:39)
40. LGPSGCGK (SEQ ID NO:40)
41. LHAGGKFD (SEQ ID NO:41)
42. LIDEARTPLIISG (SEQ ID NO:42)
43. LLNRAPTLH (SEQ ID NO:43)
44. LPDKAIDLIDE (SEQ ID NO:44)
45. LPGKLADC (SEQ ID NO:45)
46. LSGGQQQR (SEQ ID NO:46)
47. MGHVDHGKT (SEQ ID NO:47)

14. ERGITITSAAT (SEQ ID NO:14)
15. ESRRIDNQLRGR (SEQ ID NO:15)
16. FSGGQRQR (SEQ ID NO:16)
17. GEPGVGKTA (SEQ ID NO:17)
18. GFDYLRDN (SEQ ID NO:18)
19. GHNLQEHS (SEQ ID NO:19)
20. GIDLGTTNS (SEQ ID NO:20)
21. GINLLREGLD (SEQ ID NO:21)
22. GIVGLPNVGKS (SEQ ID NO:22)
23. GKSSLLNA (SEQ ID NO:23)
24. GLTGRKIIVDTYG(SEQ ID NO:24)
25. GPPGTGKTLLA (SEQ ID NO:25)
26. GPPGVGKT (SEQ ID NO:26)
27. GSGKTTLL (SEQ ID NO:27)
28. GTRIFGPV (SEQ ID NO:28)
29. IDTPGHVDFT (SEQ ID NO:29)
30. ILAHIDHGKSTL (SEQ ID NO:30)
31. INGFGRIGR (SEQ ID NO:31)
32. IREGGRTVG (SEQ ID NO:32)
33. IVGESGSGKS (SEQ ID NO:33)
34. KFSTYATWWI (SEQ ID NO:34)
48. NADFDGDQMAVH (SEQ ID NO:48)
49. NGAGKSTL (SEQ ID NO:49)
50. NLLGKRVD (SEQ ID NO:50)
51. NTDAEGRL (SEQ ID NO:51)
52. PSAVGYQPTLA (SEQ ID NO:52)
53. QRVALARA (SEQ ID NO:53)
54. QRYKGLGEM (SEQ ID NO:54)
55. RDGLKPVHRR (SEQ ID NO:55)
56. SALDVSIQA (SEQ ID NO:56)
57. SGGLHGVG (SEQ ID NO:57)
58. SGSGKSSL (SEQ ID NO:58)
59. SGSGKSTL (SEQ ID NO:59)
60. SVFAGVGERTREGND (SEQ ID NO:60)
61. TGRTHQIRVH (SEQ ID NO:61)
62. TGVSGSGKS (SEQ ID NO:62)
63. TLSGGEAQRI (SEQ ID NO:63)
64. TNKYAEGYP (SEQ ID NO:64)
65. TPRSNPATY (SEQ ID NO:65)
66. VEGDSAGG (SEQ ID NO:66) and
67. VRKRPGMYIG (SEQ ID NO:67).

5. (Currently Amended) A method as claimed in claim 1 comprising increasing the number of ~~[invariant]~~ conserved peptide sequences by increasing the relatedness among the organisms being compared.

6. (Previously Presented) A method as claimed in any one of claims 1-4 wherein the invariant sequences belong to at least one of the following proteins:

I DNA DIRECTED RNA POLYMERASE BETA CHAIN

II EXCINUCLEASE ABC SUBUNIT A

III EXCINUCLEASE ABC SUBUNIT B

IV DNA GYRASE SUBUNIT B

V ATP SYNTHASE BETA CHAIN

VI S-ADENOSYLMETHIONINE SYNTHETASE

VII GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE

VIII ELONGATION FACTOR G (EF-G)

IX ELONGATION FACTOR TU (EF-TU)

X 30S RIBOSOMAL PROTEIN S12

XI 50S RIBOSOMAL PROTEIN L12

XII 50S RIBOSOMAL PROTEIN L14

XIII VALYL tRNA SYNTHETASE (VALRS)

XIV CELL DIVISION PROTEIN FtSH HOMOLOG

XV DnaK PROTEIN (HSP70)

XVI GTP BINDING PROTEIN LepA

XVII TRANSPORTER and

XVIII OLIGOPEPTIDE TRANSPORT ATP BINDING PROTEIN OPPF.

7. (Previously Presented) A method as claimed in claim 1 wherein the said method of comparing the peptide libraries as given in step (iii) of claim 1 is carried out by following the steps:

- selecting organism names from a menu;
- iteratively comparing peptide sequences of a first organism to peptide sequences of a second organism and for matching sequences, writing sequences to a file for the first organism and to a file for the second organism.

8. (Currently Amended) A method as claimed in claim 1 wherein the said method of locating the common peptides in the original protein sequences as given in step (iv) of claim 1 is carried out by following the steps:

- selecting protein sequences;
- iteratively comparing matched peptide sequences to protein sequences;
- if the peptide is found in a protein sequence, labeling ~~labelling~~ the peptide sequence in a file associated with the protein with: a) a protein identification number (PID), b) a location in the protein sequence, and c) a name of the organism.

9. (Previously Presented) A method as claimed in claim 1 wherein the said method of creating a common peptide of variable length after removing the overlapping as given in step (v) of claim 1 is carried out by following the steps:

- iteratively comparing data on matched peptide locations;
- determining overlapping matched peptides; and
- determining extended peptide sequences based on overlapping matched peptide sequences.

10. (CANCELLED)

11. (CANCELLED)

12. (CANCELLED)